



#3

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,586
Source: OIPE
Date Processed by STIC: 6/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,586

DATE: 06/05/2001

TIME: 12:16:01

Input Set: A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

3 <110> APPLICANT: Kock, Michael
 4 Hoeger, Thomas
 5 Kroeger, Burkhard
 6 Otterbach, Bernd
 7 Lubisch, Wilfried
 8 Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586
 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: PatentIn/WordPerfect

Does Not Comply
 Corrected Diskette Needed

*know
 throughout*

OK

ERRORED SEQUENCES

148 <210> SEQ ID NO: 2
 149 <211> LENGTH: 571 *570 (see next page)*
 150 <212> TYPE: PR1
 151 <213> ORGANISM: Homo sapiens
 153 <400> SEQUENCE: 2
 155 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
 156 1 5 10 15
 157 Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
 158 20 25 30
 159 Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
 160 35 40 45
 161 Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
 162 50 55 60
 163 Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro
 164 65 70 75 80
 165 Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
 166 85 90 95
 167 Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
 168 100 105 110
 169 Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
 170 115 120 125
 171 Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
 172 130 135 140
 173 Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
 174 145 150 155 160
 175 Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
 176 165 170 175
 177 Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
 178 180 185 190

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

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179 Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu
180      195      200      205
181 Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
182      210      215      220
183 Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
184 225      230      235      240
185 Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
186      245      250      255
187 Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
188      260      265      270
189 Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
190      275      280      285
191 Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
192      290      295      300
193 Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
194 305      310      315      320
195 Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
196      325      330      335
197 Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
198      340      345      350
199 His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
200      355      360      365
201 Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
202      370      375      380
203 Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
204 385      390      395      400
205 Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
206      405      410      415
207 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
208      420      425      430
209 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
210      435      440      445
211 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
212      450      455      460
213 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
214 465      470      475      480
215 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
216      485      490      495
217 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
218      500      505      510
219 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
220      515      520      525
221 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
222      530      535      540
223 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
224 545      550      555      560
E--> 225 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp * delete stop codon
226      565      570
356 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,586

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

357 <211> LENGTH: 534 (next page)

358 <212> TYPE: PRT

359 <213> ORGANISM: Homo sapiens

361 <400> SEQUENCE: 4

363 Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys

364 1 5 10 15

365 Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr

366 20 25 30

367 Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val

368 35 40 45

369 Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu

370 50 55 60

371 Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn

372 65 70 75 80

373 Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr

374 85 90 95

375 Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile

376 100 105 110

377 Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys

378 115 120 125

379 Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val

380 130 135 140

381 Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu

382 145 150 155 160

383 Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val

384 165 170 175

385 Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu

386 180 185 190

387 Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu

388 195 200 205

389 Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln

390 210 215 220

391 Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu

392 225 230 235 240

393 Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His

394 245 250 255

395 Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro

396 260 265 270

397 Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val

398 275 280 285

399 Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln

400 290 295 300

401 Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln

402 305 310 315 320

403 Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr

404 325 330 335

405 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys

406 340 345 350

407 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp

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DATE: 06/05/2001

TIME: 12:16:01

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

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408          355          360          365
409 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
410          370          375          380
411 Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
412 385          390          395          400
413 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
414          405          410          415
415 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
416          420          425          430
417 Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
418          435          440          445
419 Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
420          450          455          460
421 Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
422 465          470          475          480
423 Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
424          485          490          495
425 Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
426          500          505          510
427 Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
428          515          520          525
E--> 429 Leu Glu Val His Leu * delete
430          530
561 <210> SEQ ID NO: 6
562 <211> LENGTH: 541 540 (next page)
563 <212> TYPE: PRT
564 <213> ORGANISM: Homo sapiens
566 <400> SEQUENCE: 6
568 Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
569 1 5 10 15
570 Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
571 20 25 30
572 Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
573 35 40 45
574 Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
575 50 55 60
576 Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr
577 65 70 75 80
578 Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln
579 85 90 95
580 Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly
581 100 105 110
582 Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala
583 115 120 125
584 Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp
585 130 135 140
586 Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile
587 145 150 155 160
588 Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp

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TIME: 12:16:01

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

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589          165          170          175
590 Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu
591          180          185          190
592 Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met
593          195          200          205
594 Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro
595          210          215          220
596 Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu
597 225          230          235          240
598 Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser
599          245          250          255
600 Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe
601          260          265          270
602 Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala
603          275          280          285
604 Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala
605          290          295          300
606 Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His
607 305          310          315          320
608 Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu
609          325          330          335
610 Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln
611          340          345          350
612 Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val
613          355          360          365
614 Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly
615          370          375          380
616 Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
617 385          390          395          400
618 Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
619          405          410          415
620 Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
621          420          425          430
622 Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
623          435          440          445
624 Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
625          450          455          460
626 Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
627 465          470          475          480
628 His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
629          485          490          495
630 Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
631          500          505          510
632 Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
633          515          520          525
E--> 634 Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu * delete
635          530          535          540
638 <210> SEQ ID NO: 7
639 <211> LENGTH: 1740

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1739 (see pp. 6-8)

RAW SEQUENCE LISTING

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DATE: 06/05/2001

TIME: 12:16:01

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

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640 <212> TYPE: DNA
641 <213> ORGANISM: Mus musculus
643 <220> FEATURE:
644 <221> NAME/KEY: CDS
645 <222> LOCATION: 112..1710
647 <400> SEQUENCE: 7
E--> 649 cccggctttc actttttctg ctgcctcggg gaacacctcg agccaactgc ttcctaactc
E--> 650 aggggtgggca gaactgacgg gatctaagct tctgcatctc tgaggagaac c atg gct,
651 Met Ala
E--> 653 cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga
654 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
W--> 655 545 550 555
E--> 656 caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc
657 Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
W--> 658 560 565 570 575
E--> 659 aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt
660 Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
W--> 661 580 585 590
E--> 662 cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt
663 Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys
W--> 664 595 600 605
E--> 665 acc ctg aac cag acc aac atc ggc aac aac aac aag ttc tat att
666 Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile
W--> 667 610 615 620
E--> 668 atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg
669 Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp
W--> 670 625 630 635
E--> 671 ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc
672 Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys
W--> 673 640 645 650 655
E--> 674 ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act
675 Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr
W--> 676 660 665 670
E--> 677 aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag
678 Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys
W--> 679 675 680 685
E--> 680 tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta
681 Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val
W--> 682 690 695 700
E--> 683 gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg
684 Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val
W--> 685 705 710 715
E--> 686 gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac
687 Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn
W--> 688 720 725 730 735
E--> 689 atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg
690 Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu
W--> 691 740 745 750
E--> 692 gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc
789

```

6059

117

165

↓
humbers

213

off

261

↓

309

357

405

453

501

549

597

645

693

741

789

RAW SEQUENCE LISTING

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Input Set : A:\es.txt

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693	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	
W--> 694				755					760				765				
E--> 695	cgt	ggc	ttc	gag	gcc	ttg	gaa	gct	cta	gag	gag	gcc	atg	aaa	aac	ccc	837
696	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	
W--> 697			770					775					780				
E--> 698	aca	ggg	gat	ggc	cag	agc	ctg	gaa	gag	ctc	tcc	tcc	tgc	ttc	tac	act	885
699	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	
W--> 700		785					790				795						
E--> 701	gtc	atc	cca	cac	aac	ttc	ggc	cgc	agc	cga	ccc	ccg	ccc	atc	aac	tcc	933
702	Val	Ile	Pro	His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	
W--> 703	800					805					810					815	
E--> 704	cct	gat	gtg	ctt	cag	gcc	aag	aag	gac	atg	ctg	ctg	gtg	cta	gcg	gac	981
705	Pro	Asp	Val	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	
W--> 706				820					825					830			
E--> 707	atc	gag	ttg	gcg	cag	acc	ttg	cag	gca	gcc	cct	ggg	gag	gag	gag	gag	1029
708	Ile	Glu	Leu	Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	
W--> 709			835					840					845				
E--> 710	aaa	gtg	gaa	gag	gtg	cca	cac	cca	ctg	gat	cga	gac	tac	cag	ctc	ctc	1077
711	Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	
W--> 712			850					855					860				
E--> 713	agg	tgc	cag	ctt	caa	ctg	ctg	gac	tcc	ggg	gag	tcc	gag	tac	aag	gca	1125
714	Arg	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	
W--> 715		865					870				875						
E--> 716	ata	cag	acc	tac	ctg	aaa	cag	act	ggc	aac	agc	tac	agg	tgc	cca	aac	1173
717	Ile	Gln	Thr	Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	
W--> 718	880				885				890					895			
E--> 719	ctg	cgg	cat	gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	1221
720	Leu	Arg	His	Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	
W--> 721				900					905					910			
E--> 722	cag	gcc	cac	tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	1269
723	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	
W--> 724			915					920					925				
E--> 725	aat	gtg	gcc	gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	1317
726	Asn	Val	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	
W--> 727			930					935					940				
E--> 728	cca	cac	tgc	ggt	ggt	cgt	gtt	ggc	aag	ggt	att	tat	ttt	gcc	tct	gag	1365
729	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	
W--> 730		945					950					955					
E--> 731	aac	agc	aag	tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	1413
732	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	
W--> 733	960				965				970					975			
E--> 734	cag	gtg	ggc	tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	1461
735	Gln	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	
W--> 736			980					985					990				
E--> 737	cac	atc	acc	atc	gat	gac	ccc	agc	ttg	aag	agt	cca	ccc	cct	ggc	ttt	1509
738	His	Ile	Thr	Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	
W--> 739			995					1000					1005				
E--> 740	gac	agc	gtc	atc	gcc	cga	ggc	caa	acc	gag	ccg	gat	ccc	gcc	cag	gac	1557
741	Asp	Ser	Val	Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	

nos.
off

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```

W--> 742          1010          1015          1020
E--> 743 att gaa ctt gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg      1605
      744 Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro
W--> 745          1025          1030          1035
E--> 746 cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa      1653
      747 Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu
W--> 748 1040          1045          1050          1055
E--> 749 tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag      1701
      750 Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu
W--> 751          1060          1065          1070
E--> 752 att cac ctc taagctgctt gccctcccta ggtccaagcc      1740
E--> 753 Ile His Leu
      944 <210> SEQ ID NO: 10
      945 <211> LENGTH: 528
      946 <212> TYPE: DNA PRT
      947 <213> ORGANISM: Mus musculus
      949 <400> SEQUENCE: 10
      951 Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
      952   1          5          10          15
      953 Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
      954          20          25          30
      955 Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
      956          35          40          45
      957 Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
      958          50          55          60
      959 Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
      960          65          70          75          80
      961 Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
      962          85          90          95
      963 Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
      964          100          105          110
      965 Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
      966          115          120          125
      967 Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
      968          130          135          140
      969 Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
      970          145          150          155          160
      971 Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
      972          165          170          175
      973 Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
      974          180          185          190
      975 Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
      976          195          200          205
      977 Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
      978          210          215          220
      979 Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
      980          225          230          235          240
      981 Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
      982          245          250          255

```

nos.
off
↓

RAW SEQUENCE LISTING

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```

983 His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
984      260      265      270
985 Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
986      275      280      285
987 Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu
988      290      295      300
989 Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
990 305      310      315      320
991 Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
992      325      330      335
993 Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
994      340      345      350
995 Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
996      355      360      365
997 Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
998      370      375      380
999 Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
1000 385      390      395      400
1001 Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
1002      405      410      415
1003 Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
1004      420      425      430
1005 Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
1006      435      440      445
1007 Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
1008      450      455      460
1009 Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
1010 465      470      475      480
1011 Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
1012      485      490      495
1013 Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
1014      500      505      510
1015 Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
E--> 1016      515      520      525
1241 <210> SEQ ID NO: 19
1242 <211> LENGTH: 17
1243 <212> TYPE: PRT
1244 <213> ORGANISM: artificial sequence
1246 <220> FEATURE:
1247 <223> OTHER INFORMATION: part-sequence motif 5
1249 <220> FEATURE:
1250 <221> NAME/KEY: VARIANT
1251 <222> LOCATION: 2..4, 6..7, 9, 13, 15..16
1252 <223> OTHER INFORMATION: amino acid residues 2 to 4, 6 to 7, 9, 13 and 15 to 16 may
be any
1253      amino
1254      acid
E--> 1256 <400> 19 ← insert
1258 Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
1259      5      10      15

```

RAW SEQUENCE LISTING

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1261 Leu
 1264 <210> SEQ ID NO: 20
 1265 <211> LENGTH: 11
 1266 <212> TYPE: PRT
 1267 <213> ORGANISM: artificial sequence
 E--> 1269 <200> *invalid use <220>, instead*
 1270 <223> OTHER INFORMATION: part-sequence motif 6
 OK-> 1272 <220> FEATURE:
 1273 <221> NAME/KEY: VARIANT
 1274 <222> LOCATION: 2..4, 6
 1275 <223> OTHER INFORMATION: amino acid residues 2 to 4 and 6 may be any amino acid
 1277 <400> SEQUENCE: 20
 OK 1279 Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1280 5 10
 1461 <210> SEQ ID NO: 31
 1462 <211> LENGTH: 10
 1463 <212> TYPE: PRT
 1464 <213> ORGANISM: Arabidopsis thaliana
 E--> 1466
 1468 Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 1469 5 10
 1471 <210> SEQ ID NO: 32
 1472 <211> LENGTH: 39
 1473 <212> TYPE: DNA
 1474 <213> ORGANISM: Homo sapiens
 1476 <220> FEATURE:
 1477 <221> NAME/KEY: CDS
 1478 <222> LOCATION: 1..39
 E--> 1480
 1482 gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg 39
 1483 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1484 5 10
 1487 <210> SEQ ID NO: 33
 1488 <211> LENGTH: 13
 1489 <212> TYPE: PRT
 1490 <213> ORGANISM: Homo sapiens
 E--> 1492
 1494 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1495 5 10

see following pages for explanation

<210> 29
 <211> 7
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> 2..4
 <223> amino acid residues 2 to 4 may be any amino acid residue

<400> 29 ← insert
 Gly Xaa Xaa Xaa Gly Lys Gly
 5

<210> 30
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PARP zinc finger sequence motif

<220>
 <221> VARIANT
 <222> 2..3, 5..34, 36..37
 <223> amino acid residues 2 to 3, 5 to 34 and 36 to 37 may be any amino acid residue; residues 33 and 34 may be present or absent

<400> 30 ← insert
 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa His Xaa Xaa Cys
 35

<210> 31
 <211> 10
 <212> PRT
 <213> Arabidopsis thaliana

<400> 31 ← insert

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 5 10

<210> 32
 <211> 39
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..39

<400> 32 ← insert

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 5 10

39

<210> 33
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 33 ← insert

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 5 10

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Input Set : A:\es.txt

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L:225 M:342 E: Invalid Stop Code On Error, STOP CODON:*
 L:241 M:112 C: (48) String data converted to lower case,
 L:242 M:112 C: (48) String data converted to lower case,
 L:243 M:112 C: (48) String data converted to lower case,
 L:244 M:112 C: (48) String data converted to lower case,
 L:245 M:112 C: (48) String data converted to lower case,
 L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:248 M:112 C: (48) String data converted to lower case,
 L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:251 M:112 C: (48) String data converted to lower case,
 L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:254 M:112 C: (48) String data converted to lower case,
 L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:257 M:112 C: (48) String data converted to lower case,
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:260 M:112 C: (48) String data converted to lower case,
 L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:263 M:112 C: (48) String data converted to lower case,
 L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:266 M:112 C: (48) String data converted to lower case,
 L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:269 M:112 C: (48) String data converted to lower case,
 L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:272 M:112 C: (48) String data converted to lower case,
 L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:275 M:112 C: (48) String data converted to lower case,
 L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:278 M:112 C: (48) String data converted to lower case,
 L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:281 M:112 C: (48) String data converted to lower case,
 L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:284 M:112 C: (48) String data converted to lower case,
 L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:287 M:112 C: (48) String data converted to lower case,
 L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:290 M:112 C: (48) String data converted to lower case,
 L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:293 M:112 C: (48) String data converted to lower case,
 L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:296 M:112 C: (48) String data converted to lower case,
 L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:299 M:112 C: (48) String data converted to lower case,
 L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:302 M:112 C: (48) String data converted to lower case,
 L:304 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:305 M:112 C: (48) String data converted to lower case,
 L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:308 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:311 M:112 C: (48) String data converted to lower case,
 L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:314 M:112 C: (48) String data converted to lower case,
 L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:317 M:112 C: (48) String data converted to lower case,
 L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:320 M:112 C: (48) String data converted to lower case,
 L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:323 M:112 C: (48) String data converted to lower case,
 L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:326 M:112 C: (48) String data converted to lower case,
 L:328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:329 M:112 C: (48) String data converted to lower case,
 L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:332 M:112 C: (48) String data converted to lower case,
 L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:335 M:112 C: (48) String data converted to lower case,
 L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:338 M:112 C: (48) String data converted to lower case,
 L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:341 M:112 C: (48) String data converted to lower case,
 L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:344 M:112 C: (48) String data converted to lower case,
 L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:347 M:112 C: (48) String data converted to lower case,
 L:348 M:112 C: (48) String data converted to lower case,
 L:349 M:112 C: (48) String data converted to lower case,
 L:350 M:112 C: (48) String data converted to lower case,
 L:351 M:112 C: (48) String data converted to lower case,
 L:352 M:112 C: (48) String data converted to lower case,
 L:353 M:112 C: (48) String data converted to lower case,
 L:429 M:342 E: Invalid Stop Code On Error, STOP CODON:*
 L:444 M:112 C: (48) String data converted to lower case,
 L:445 M:112 C: (48) String data converted to lower case,
 L:446 M:112 C: (48) String data converted to lower case,
 L:447 M:112 C: (48) String data converted to lower case,
 L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:450 M:112 C: (48) String data converted to lower case,
 L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:453 M:112 C: (48) String data converted to lower case,
 L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:456 M:112 C: (48) String data converted to lower case,
 L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:459 M:112 C: (48) String data converted to lower case,
 L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:462 M:112 C: (48) String data converted to lower case,
 L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:465 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:468 M:112 C: (48) String data converted to lower case,
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:471 M:112 C: (48) String data converted to lower case,
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:474 M:112 C: (48) String data converted to lower case,
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:477 M:112 C: (48) String data converted to lower case,
L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:480 M:112 C: (48) String data converted to lower case,
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:483 M:112 C: (48) String data converted to lower case,
L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:486 M:112 C: (48) String data converted to lower case,
L:488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:489 M:112 C: (48) String data converted to lower case,
L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:492 M:112 C: (48) String data converted to lower case,
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:495 M:112 C: (48) String data converted to lower case,
L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:498 M:112 C: (48) String data converted to lower case,
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:501 M:112 C: (48) String data converted to lower case,
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:504 M:112 C: (48) String data converted to lower case,
L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:507 M:112 C: (48) String data converted to lower case,
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:510 M:112 C: (48) String data converted to lower case,
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:513 M:112 C: (48) String data converted to lower case,
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:516 M:112 C: (48) String data converted to lower case,
L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:519 M:112 C: (48) String data converted to lower case,
L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:522 M:112 C: (48) String data converted to lower case,
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:525 M:112 C: (48) String data converted to lower case,
L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:528 M:112 C: (48) String data converted to lower case,
L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:531 M:112 C: (48) String data converted to lower case,
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:534 M:112 C: (48) String data converted to lower case,
L:536 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:537 M:112 C: (48) String data converted to lower case,
L:539 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

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Input Set : A:\es.txt

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L:540 M:112 C: (48) String data converted to lower case,
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:543 M:112 C: (48) String data converted to lower case,
L:545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:546 M:112 C: (48) String data converted to lower case,
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:549 M:112 C: (48) String data converted to lower case,
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:552 M:112 C: (48) String data converted to lower case,
L:553 M:112 C: (48) String data converted to lower case,
L:554 M:112 C: (48) String data converted to lower case,
L:555 M:112 C: (48) String data converted to lower case,
L:556 M:112 C: (48) String data converted to lower case,
L:557 M:112 C: (48) String data converted to lower case,
L:558 M:112 C: (48) String data converted to lower case,
L:634 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:649 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:59 SEQ:7
L:649 M:112 C: (48) String data converted to lower case,
L:650 M:254 E: No. of Bases conflict, LENGTH:Input:117 Counted:116 SEQ:7
L:650 M:112 C: (48) String data converted to lower case,
L:653 M:254 E: No. of Bases conflict, LENGTH:Input:165 Counted:164 SEQ:7
L:653 M:112 C: (48) String data converted to lower case,
L:655 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:656 M:254 E: No. of Bases conflict, LENGTH:Input:213 Counted:212 SEQ:7
L:656 M:112 C: (48) String data converted to lower case,
L:658 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:659 M:254 E: No. of Bases conflict, LENGTH:Input:261 Counted:260 SEQ:7
L:659 M:112 C: (48) String data converted to lower case,
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:662 M:254 E: No. of Bases conflict, LENGTH:Input:309 Counted:308 SEQ:7
L:662 M:112 C: (48) String data converted to lower case,
L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:665 M:254 E: No. of Bases conflict, LENGTH:Input:357 Counted:356 SEQ:7
L:665 M:112 C: (48) String data converted to lower case,
L:667 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:668 M:254 E: No. of Bases conflict, LENGTH:Input:405 Counted:404 SEQ:7
L:668 M:112 C: (48) String data converted to lower case,
L:670 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:671 M:254 E: No. of Bases conflict, LENGTH:Input:453 Counted:452 SEQ:7
L:671 M:112 C: (48) String data converted to lower case,
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:674 M:254 E: No. of Bases conflict, LENGTH:Input:501 Counted:500 SEQ:7
L:674 M:112 C: (48) String data converted to lower case,
L:676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:677 M:254 E: No. of Bases conflict, LENGTH:Input:549 Counted:548 SEQ:7
L:677 M:112 C: (48) String data converted to lower case,
L:679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:680 M:254 E: No. of Bases conflict, LENGTH:Input:597 Counted:596 SEQ:7
L:680 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt

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L:682 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:683 M:254 E: No. of Bases conflict, LENGTH:Input:645 Counted:644 SEQ:7
L:683 M:112 C: (48) String data converted to lower case,
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:686 M:254 E: No. of Bases conflict, LENGTH:Input:693 Counted:692 SEQ:7
L:686 M:112 C: (48) String data converted to lower case,
L:688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:689 M:254 E: No. of Bases conflict, LENGTH:Input:741 Counted:740 SEQ:7
L:689 M:112 C: (48) String data converted to lower case,
L:691 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:789 Counted:788 SEQ:7
L:692 M:112 C: (48) String data converted to lower case,
L:694 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:695 M:254 E: No. of Bases conflict, LENGTH:Input:837 Counted:836 SEQ:7
L:695 M:112 C: (48) String data converted to lower case,
L:697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:698 M:254 E: No. of Bases conflict, LENGTH:Input:885 Counted:884 SEQ:7
L:698 M:112 C: (48) String data converted to lower case,
L:700 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:701 M:254 E: No. of Bases conflict, LENGTH:Input:933 Counted:932 SEQ:7
L:701 M:112 C: (48) String data converted to lower case,
L:703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:704 M:254 E: No. of Bases conflict, LENGTH:Input:981 Counted:980 SEQ:7
L:704 M:112 C: (48) String data converted to lower case,
L:706 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:707 M:254 E: No. of Bases conflict, LENGTH:Input:1029 Counted:1028 SEQ:7
L:707 M:112 C: (48) String data converted to lower case,
L:709 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:710 M:254 E: No. of Bases conflict, LENGTH:Input:1077 Counted:1076 SEQ:7
L:710 M:112 C: (48) String data converted to lower case,
L:712 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:713 M:254 E: No. of Bases conflict, LENGTH:Input:1125 Counted:1124 SEQ:7
L:713 M:112 C: (48) String data converted to lower case,
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:716 M:254 E: No. of Bases conflict, LENGTH:Input:1173 Counted:1172 SEQ:7
L:716 M:112 C: (48) String data converted to lower case,
L:718 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:719 M:254 E: No. of Bases conflict, LENGTH:Input:1221 Counted:1220 SEQ:7
L:719 M:112 C: (48) String data converted to lower case,
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:722 M:254 E: No. of Bases conflict, LENGTH:Input:1269 Counted:1268 SEQ:7
L:722 M:112 C: (48) String data converted to lower case,
L:724 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:725 M:254 E: No. of Bases conflict, LENGTH:Input:1317 Counted:1316 SEQ:7
L:725 M:112 C: (48) String data converted to lower case,
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:728 M:254 E: No. of Bases conflict, LENGTH:Input:1365 Counted:1364 SEQ:7
L:728 M:112 C: (48) String data converted to lower case,
L:730 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

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PATENT APPLICATION: US/09/701,586

DATE: 06/05/2001

TIME: 12:16:02

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

L:731 M:254 E: No. of Bases conflict, LENGTH:Input:1413 Counted:1412 SEQ:7
L:731 M:112 C: (48) String data converted to lower case,
L:733 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:734 M:254 E: No. of Bases conflict, LENGTH:Input:1461 Counted:1460 SEQ:7
L:734 M:112 C: (48) String data converted to lower case,
L:736 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:737 M:254 E: No. of Bases conflict, LENGTH:Input:1509 Counted:1508 SEQ:7
L:737 M:112 C: (48) String data converted to lower case,
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:740 M:254 E: No. of Bases conflict, LENGTH:Input:1557 Counted:1556 SEQ:7
L:740 M:112 C: (48) String data converted to lower case,
L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:743 M:254 E: No. of Bases conflict, LENGTH:Input:1605 Counted:1604 SEQ:7
L:743 M:112 C: (48) String data converted to lower case,
L:745 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:746 M:254 E: No. of Bases conflict, LENGTH:Input:1653 Counted:1652 SEQ:7
L:746 M:112 C: (48) String data converted to lower case,
L:748 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:749 M:254 E: No. of Bases conflict, LENGTH:Input:1701 Counted:1700 SEQ:7
L:749 M:112 C: (48) String data converted to lower case,
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:752 M:254 E: No. of Bases conflict, LENGTH:Input:1740 Counted:1739 SEQ:7
L:752 M:112 C: (48) String data converted to lower case,
L:753 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1740 Found:1739 SEQ:7
L:843 M:112 C: (48) String data converted to lower case,
L:845 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:846 M:112 C: (48) String data converted to lower case,
L:848 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:849 M:112 C: (48) String data converted to lower case,
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:852 M:112 C: (48) String data converted to lower case,
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:855 M:112 C: (48) String data converted to lower case,
L:857 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:858 M:112 C: (48) String data converted to lower case,
L:860 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:861 M:112 C: (48) String data converted to lower case,
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:864 M:112 C: (48) String data converted to lower case,
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:867 M:112 C: (48) String data converted to lower case,
L:869 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:870 M:112 C: (48) String data converted to lower case,
L:872 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:873 M:112 C: (48) String data converted to lower case,
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:876 M:112 C: (48) String data converted to lower case,
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:879 M:112 C: (48) String data converted to lower case,

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Input Set : **A:\es.txt**Output Set: **C:\CRF3\06052001\I701586.raw**

L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:882 M:112 C: (48) String data converted to lower case,
L:884 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:885 M:112 C: (48) String data converted to lower case,
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:888 M:112 C: (48) String data converted to lower case,
L:890 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:891 M:112 C: (48) String data converted to lower case,
L:893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:894 M:112 C: (48) String data converted to lower case,
L:896 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:897 M:112 C: (48) String data converted to lower case,
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:900 M:112 C: (48) String data converted to lower case,
L:902 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:903 M:112 C: (48) String data converted to lower case,
L:905 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:906 M:112 C: (48) String data converted to lower case,
L:908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:909 M:112 C: (48) String data converted to lower case,
L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:912 M:112 C: (48) String data converted to lower case,
L:914 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:915 M:112 C: (48) String data converted to lower case,
L:917 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:918 M:112 C: (48) String data converted to lower case,
L:920 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:921 M:112 C: (48) String data converted to lower case,
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:924 M:112 C: (48) String data converted to lower case,
L:926 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:927 M:112 C: (48) String data converted to lower case,
L:929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:930 M:112 C: (48) String data converted to lower case,
L:932 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:933 M:112 C: (48) String data converted to lower case,
L:935 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:936 M:112 C: (48) String data converted to lower case,
L:938 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:939 M:112 C: (48) String data converted to lower case,
L:941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:942 M:112 C: (48) String data converted to lower case,
L:1016 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:0 SEQ:10
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I701586.raw

L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:18
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1269 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1466 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:28
L:1480 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:28
L:1492 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:28
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (33) Counted (31)